WHAT IS CLAIMED IS:

1. A method for predicting the likelihood that an individual will develop multiple sclerosis, comprising:

a) obtaining a nucleic acid sample from an individual to be assessed; and

b) determining the nucleotide present at the nucleotide position corresponding to position 226 of the native CD24 gene in the individual which sequence corresponds to SEQ ID NO: 1,

wherein the presence of an thymidine at position 226 indicates that the individual has a greater likelihood of being diagnosed with multiple sclerosis than an individual having a cytosine at that position.

2. A method for predicting the likelihood that an individual will develop multiple sclerosis, comprising:

a) obtaining a nucleic acid sample from an individual to be assessed; and

b) determining the nucleotide present at the nucleotide position corresponding to position 1110 of the native CD24 gene in the individual which sequence corresponds to SEQ ID NO: 1,

wherein the presence of a guanine at position 1110 indicates that the individual has a greater likelihood of being diagnosed with multiple sclerosis than an individual having an adenine at that position.

3. The method according to either of claims 1 or 2, wherein the individual is an individual at risk for development multiple sclerosis based on the presence of an allelic variant of HLA.

4. The method according to either of claims 1 or 2, wherein the individual exhibits clinical symptoms of multiple sclerosis.

5. The method according to either of claims 1 or 2, wherein at least one blood relative of the individual has been diagnosed with multiple sclerosis.

6. A method for predicting the likelihood that an individual who has been diagnosed with multiple sclerosis will experience rapid progression of multiple sclerosis, comprising:

a) obtaining a nucleic acid sample from an individual to be assessed; and

b) determining the nucleotide present at the nucleotide position corresponding to position 226 of the native CD24 gene in the individual which sequence corresponds to SEQ ID NO: 1,

wherein the presence of an thymidine at position 226 indicates that the individual has a greater likelihood of experiencing rapid progression of multiple sclerosis than an individual diagnosed with multiple sclerosis and having an cytosine at that position.

7. A method for predicting the likelihood that an individual who has been diagnosed with multiple sclerosis will experience rapid progression of multiple sclerosis, comprising:

a) obtaining a nucleic acid sample from an individual to be assessed; and

b) determining if there is a deletion at positions 1580 and 1581 of the native CD24 gene in the individual, which sequence corresponds to SEQ ID NO: 1,

wherein deletions of TG at positions 1580 and 1581 indicate that the individual has a greater likelihood of experiencing rapid progression of multiple sclerosis than an individual diagnosed with multiple sclerosis and having TG at those positions.

8. A method of diagnosing or aiding in the diagnosis of multiple sclerosis in an individual comprising:

a) obtaining a nucleic acid sample from the individual;

b) determining the HLA genotype of the individual; and

c) determining the nucleotide present at nucleotide position 226 of the CD24 gene,

wherein the presence of the HLA-DR2 genotype together with the presence of a thymidine at position 226 of the CD24 gene is indicative that the individual is more likely to develop multiple sclerosis as compared with an individual lacking the HLA-DR2 genotype and having a cytosine at position 226 of the CD24 gene.

9. A method of diagnosing or aiding in the diagnosis of multiple sclerosis in an individual comprising:

a) obtaining a nucleic acid sample from the individual;

b) determining the HLA genotype of the individual; and

c) determining the nucleotide present at nucleotide position 1110 of the CD24 gene,

wherein the presence of the HLA-DR2 genotype together with the presence of a guanine at position 1110 of the CD24 gene is indicative that the individual is more likely to develop multiple sclerosis as compared with an individual lacking the HLA-DR2 genotype and having an adenine at position 1110 of the CD24 gene.

10. A method for predicting the likelihood that an individual will develop multiple sclerosis, comprising:

a) obtaining a cell sample from an individual to be assessed;

b) determining the level of cell surface expression of CD24 protein on the surface of said cells; and

c) determining a base-line level of cell surface expression of the CD24 protein on control cells,

wherein an increased level of expression of CD24 on the cells isolated from the individual as compared with the control cells indicates that the individual has a thymidine at position 226 of the CD24 gene, and therefore has a greater likelihood of being diagnosed with multiple sclerosis than an individual having a cytosine at that position.

11. A method for predicting the likelihood that an individual will develop multiple sclerosis, comprising:

a) obtaining a cell sample from an individual to be assessed;

b) determining the level of cell surface expression of CD24 protein on the surface of said cells; and

c) determining a base-line level of cell surface expression of the CD24 protein on control cells,

wherein an increased level of expression of CD24 on the cells isolated from the individual as compared with the control cells indicates that the individual has a guanine at position 1110 of the CD24 gene, and therefore has a greater likelihood

of being diagnosed with multiple sclerosis than an individual having a adenine at that position.

12. The method according to either of claims 10 or 11, wherein the cell sample comprises peripheral blood lymphocytes.

13. The method according to either of claims 10 or 11, wherein the cell sample comprises T lymphocytes.

14. The method according to either of claims 10 or 11, wherein the individual is an individual at risk for development multiple sclerosis based on the presence of an allelic variant of HLA.

15. The method according to either of claims 10 or 11, wherein the individual exhibits clinical symptoms of multiple sclerosis.

16. The method according to either of claims 10 or 11, wherein at least one blood relative of the individual has been diagnosed with multiple sclerosis.

17. A method for predicting the likelihood that an individual will develop multiple sclerosis, comprising:

a) obtaining a nucleic acid sample from an individual to be assessed;

b) screening the entire nucleotide sequence encoding the human CD24; and

c) detecting the presence of one ore more polymorphisms of the CD24,

wherein the presence of an thymidine at position 226, and the presence of at least one other variant allele in the polynucleotide encoding CD24 that has been shown to have a positive correlation with increased risk for developing MS based on both population study and on transmission disequilibrium analysis, indicates that the individual has a greater likelihood of developing multiple sclerosis than an

individual having a cytosine at position 226 and lacking any other variant alleles in the polynucleotide encoding CD24 that has been shown to have a positive correlation with increased risk for developing MS based on both population study and on transmission disequilibrium analysis.

18. A method for predicting the likelihood that an individual will develop multiple sclerosis, comprising:

a) obtaining a nucleic acid sample from an individual to be assessed;

b) screening the entire nucleotide sequence encoding the human CD24; and

c) detecting the presence of one ore more polymorphisms of the CD24,

wherein the presence of an guanine at position 1110, and the presence of at least one other variant allele in the polynucleotide encoding CD24 that has been shown to have a positive correlation with increased risk for developing MS based on both population study and on transmission disequilibrium analysis, indicates that the individual has a greater likelihood of developing multiple sclerosis than an individual having an adenine at position 1110 and lacking any other variant alleles in the polynucleotide encoding CD24 that has been shown to have a positive correlation with increased risk for developing MS based on both population study and on transmission disequilibrium analysis.